

0280
Errors Corrected by the STIC Systems Branch

01PE
#2

Serial Number: 09/823,373

CRF Processing Date: _____
 Edited by: _____
 Verified by: _____ (STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/823,373

DATE: 04/20/2001
 TIME: 14:10:46

Input Set : A:\Cpg.pto
 Output Set: N:\CRF3\04202001\I823373.raw

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4 <110> APPLICANT: Chauhan, Sarita
5     DiCosimo, Robert
6     Payne, Mark
7     Gavagan, John
8     Fallon, Robert
10 <120> TITLE OF INVENTION: Isolation and Expression of a Gene for Nitrilase from
11     Acidovorax Facilis 72W
13 <130> FILE REFERENCE: BC-1032 US NA
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/823,373
C--> 16 <141> CURRENT FILING DATE: 2001-03-30
18 <150> PRIOR APPLICATION NUMBER: 60/193,707
19 <151> PRIOR FILING DATE: 2000-03-31
21 <160> NUMBER OF SEQ ID NOS: 32
23 <170> SOFTWARE: Microsoft Office 97
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 17
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial Sequence
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31 <223> OTHER INFORMATION: Description of Artificial Sequence: Forward primer
32     (1F)
34 <220> FEATURE:
35 <223> OTHER INFORMATION: K= G or T, M= A or C, S= G or C, Y= C or T
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41 <210> SEQ ID NO: 2
42 <211> LENGTH: 17
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial Sequence
46 <220> FEATURE:
47 <223> OTHER INFORMATION: Description of Artificial Sequence: Reverse primer
48     (7R)
50 <220> FEATURE:
51 <223> OTHER INFORMATION: S= G or C, H= A or C or T, M= A or C, R= A or G,
52     Y= C or T
54 <400> SEQUENCE: 2
55 ggccasshtg mrayrtg 17
58 <210> SEQ ID NO: 3
59 <211> LENGTH: 385
60 <212> TYPE: DNA
61 <213> ORGANISM: Acidovorax facilis
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65 gaattcggtg gagctagggtg acgaccgtat gcgtcgccctc cagctggccg cgcgcgcgcaa 120
66 caaaatcgca ctcgtcattg gctattcgga gcgggaagcc ggatcgcgct atctgagcca 180
67 ggtgttcacg gacgagcggtg gcgagatcgt tgccaatcgg cgcaagctga agccacaca 240
68 cgttgagcgt acgatctacg gcgaaggcaa cggaaccgat ttcctcacgc acgacttcgc 300

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70 gatgtacagc ctcggtgagc aggtc                                     385
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74 <211> LENGTH: 1110
75 <212> TYPE: DNA
76 <213> ORGANISM: Acidovorax facilis
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81 gcgagtctga tcgctttccc ggaagtattc attccgggct acccctattg ggcgtggctc 180
82 ggcgacgtga agtacagcct aagctttact tcacgctatc acgagaattc gttggagcta 240
83 ggtgacgacc gtatgcgctg cctccagctg gccgcgcgcc gcaacaaaat cgcactcgtc 300
84 atgggctatt cggagcggga agccggatcg cgctatctga gccaggtgtt catcgacgag 360
85 cgtggcgaga tcgttgccaa tcggcgcaag ctgaagccca cacacgttga gcgtacgac 420
86 tacggcgaag gcaacggaac cgatttcctc acgcacgact tcgcgttcgg acgcgtcggt 480
87 ggattgaact gctgggaaca tttccaaccg ctacgcaagt tcatgatgta cagcctcggt 540
88 gacgaggtcc acgttgcatc gtggccggcg atgtcccctc ttcagccgga tgttttccaa 600
89 ctgagcatcg aagccaacgc gacggtcacc cgctcgtagc caatcgaagg ccaaaccctt 660
90 gtgctttgct cgacgcaggt gatcggaact agcgcgatcg aaacgttctg cctcaacgac 720
91 gaacagcgcg cactgttgcc gcaaggatgt ggctgggccc gcatttacgg cccggatgga 780
92 agcgagcttg cgaagcctct ggcggaagat gctgagggga tcttgtagcg agagatcgat 840
93 ctggagcaga ttctgctggc gaaggctgga gccgatccgg tcgggcacta ttcgcgccct 900
94 gacgtgctgt cgggtccagt cgacccgcgc aatcatacgc cagttcatcg catcggcatt 960
95 gacggtcgct tggatgtgaa taccgcagc cgcggtgaga atttccgact gcgacaagcg 1020
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97 ctggctgaag aaccggtccc agcaaagtag                                     1110
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101 <211> LENGTH: 369
102 <212> TYPE: PRT
103 <213> ORGANISM: Acidovorax facilis
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107 1 5 10 15
109 Pro Val Trp Leu Asp Ala Asp Ala Thr Ile Asp Lys Ser Ile Gly Ile
110 20 25 30
112 Ile Glu Glu Ala Ala Gln Lys Gly Ala Ser Leu Ile Ala Phe Pro Glu
113 35 40 45
115 Val Phe Ile Pro Gly Tyr Pro Tyr Trp Ala Trp Leu Gly Asp Val Lys
116 50 55 60
118 Tyr Ser Leu Ser Phe Thr Ser Arg Tyr His Glu Asn Ser Leu Glu Leu
119 65 70 75 80
121 Gly Asp Asp Arg Met Arg Arg Leu Gln Leu Ala Ala Arg Arg Asn Lys
122 85 90 95
124 Ile Ala Leu Val Met Gly Tyr Ser Glu Arg Glu Ala Gly Ser Arg Tyr
125 100 105 110
127 Leu Ser Gln Val Phe Ile Asp Glu Arg Gly Glu Ile Val Ala Asn Arg
128 115 120 125
130 Arg Lys Leu Lys Pro Thr His Val Glu Arg Thr Ile Tyr Gly Glu Gly
131 130 135 140

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133 Asn Gly Thr Asp Phe Leu Thr His Asp Phe Ala Phe Gly Arg Val Gly
134 145          150          155          160
136 Gly Leu Asn Cys Trp Glu His Phe Gln Pro Leu Ser Lys Phe Met Met
137          165          170          175
139 Tyr Ser Leu Gly Glu Gln Val His Val Ala Ser Trp Pro Ala Met Ser
140          180          185          190
142 Pro Leu Gln Pro Asp Val Phe Gln Leu Ser Ile Glu Ala Asn Ala Thr
143          195          200          205
145 Val Thr Arg Ser Tyr Ala Ile Glu Gly Gln Thr Phe Val Leu Cys Ser
146          210          215          220
148 Thr Gln Val Ile Gly Pro Ser Ala Ile Glu Thr Phe Cys Leu Asn Asp
149 225          230          235          240
151 Glu Gln Arg Ala Leu Leu Pro Gln Gly Cys Gly Trp Ala Arg Ile Tyr
152          245          250          255
154 Gly Pro Asp Gly Ser Glu Leu Ala Lys Pro Leu Ala Glu Asp Ala Glu
155          260          265          270
157 Gly Ile Leu Tyr Ala Glu Ile Asp Leu Glu Gln Ile Leu Leu Ala Lys
158          275          280          285
160 Ala Gly Ala Asp Pro Val Gly His Tyr Ser Arg Pro Asp Val Leu Ser
161          290          295          300
163 Val Gln Phe Asp Pro Arg Asn His Thr Pro Val His Arg Ile Gly Ile
164 305          310          315          320
166 Asp Gly Arg Leu Asp Val Asn Thr Arg Ser Arg Val Glu Asn Phe Arg
167          325          330          335
169 Leu Arg Gln Ala Ala Glu Gln Glu Arg Gln Ala Ser Lys Arg Leu Gly
170          340          345          350
172 Thr Lys Leu Phe Glu Gln Ser Leu Leu Ala Glu Glu Pro Val Pro Ala
173          355          360          365
175 Lys
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180 <211> LENGTH: 27
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
187 <400> SEQUENCE: 6
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191 <210> SEQ ID NO: 7
192 <211> LENGTH: 28
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
196 <220> FEATURE:
197 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
199 <400> SEQUENCE: 7
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203 <210> SEQ ID NO: 8
204 <211> LENGTH: 31
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence

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216 <211> LENGTH: 23
217 <212> TYPE: DNA
218 <213> ORGANISM: Artificial Sequence
220 <220> FEATURE:
221 <223> OTHER INFORMATION: Description of Artificial Sequence:Primer
223 <400> SEQUENCE: 9
224 ttatggctac ttgctggga ccg                                         23
227 <210> SEQ ID NO: 10
228 <211> LENGTH: 29
229 <212> TYPE: DNA
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232 <220> FEATURE:
233 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
235 <400> SEQUENCE: 10
236 tacatatggt ttcgtataac agcaagttc                                   29
239 <210> SEQ ID NO: 11
240 <211> LENGTH: 26
241 <212> TYPE: DNA
242 <213> ORGANISM: Artificial Sequence
244 <220> FEATURE:
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248 catctcgaga tggtttcgta taacag                                     26
251 <210> SEQ ID NO: 12
252 <211> LENGTH: 23
253 <212> TYPE: DNA
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264 <211> LENGTH: 1110
265 <212> TYPE: DNA
266 <213> ORGANISM: Acidovorax facilis
268 <400> SEQUENCE: 13
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270 gacgcagacg caacgatcga caagtcgacg ggcacatcgc aagaagctgc ccaaaagggc 120
271 gcgagtcctga tcgctttccc ggaagtattc attccgggct acccctattg ggcgtggctc 180
272 ggcgacgtga agtacagcct aagctttact tcacgctatc acgagaattc gttggagcta 240
273 ggtgacgacc gtatgcgtcg cctccagctg gccgcgcgcc gcaacaaaat cgcactcgtc 300
274 atgggctatt cggagcggga agccggatcg cgctatctga gccaggtgtt catcgacgag 360
275 cgtggcgaga tcgttgccaa tcggcgcaag ctgaagccca cacacgttga gcgtacgata 420
276 tacggcgaa gcaacggaac cgatttcctc acgcacgact tcgcgttcgg acgcgtcggg 480

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277 ggattgaact gctgggaaca ttccaaccg ctcagcaagt tcatgatgta cagcctcgg 540
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279 ctgagcatcg aagccaacgc gacggtcacc cgctcgtacg caatcgaagg ccaaaccctt 660
280 gtgctttgct cgacgcagggt gatcggacct agcgcgatcg aaacgttctg cctcaacgac 720
281 gaacagcgcg cactgttgcc gcaaggatgt ggctgggagc gcatttacgg cccggatgga 780
282 agcgagcttg cgaagcctct ggccgaagat gctgagggga tcttgtagcg agagatcgat 840
283 ctggagcaga ttctgctggc gaaggctgga gccgatccgg tcgggcaacta ttgcgggcct 900
284 gacgtgctgt cgggccagtt cgacccgcgc aatcatacgc cagttcatcg catcggcatt 960
285 gacggtcgct tggatgtgaa taccgcagc cgcgtggaga atttccgact gcgacaagcg 1020
286 gctgagcagg agcgtcaggc atccaagcgg ctcggaacga aactctttga acaatccctt 1080
287 ctggctgaag aaccgggtccc agcaaagtag                               1110
290 <210> SEQ ID NO: 14
291 <211> LENGTH: 369
292 <212> TYPE: PRT
293 <213> ORGANISM: Acidovorax facilis
295 <400> SEQUENCE: 14
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299 Pro Val Trp Leu Asp Ala Asp Ala Thr Ile Asp Lys Ser Ile Gly Ile
300             20             25             30
302 Ile Glu Glu Ala Ala Gln Lys Gly Ala Ser Leu Ile Ala Phe Pro Glu
303             35             40             45
305 Val Phe Ile Pro Gly Tyr Pro Tyr Trp Ala Trp Leu Gly Asp Val Lys
306             50             55             60
308 Tyr Ser Leu Ser Phe Thr Ser Arg Tyr His Glu Asn Ser Leu Glu Leu
309             65             70             75             80
311 Gly Asp Asp Arg Met Arg Arg Leu Gln Leu Ala Ala Arg Arg Asn Lys
312             85             90             95
314 Ile Ala Leu Val Met Gly Tyr Ser Glu Arg Glu Ala Gly Ser Arg Tyr
315             100            105            110
317 Leu Ser Gln Val Phe Ile Asp Glu Arg Gly Glu Ile Val Ala Asn Arg
318             115            120            125
320 Arg Lys Leu Lys Pro Thr His Val Glu Arg Thr Ile Tyr Gly Glu Gly
321             130            135            140
323 Asn Gly Thr Asp Phe Leu Thr His Asp Phe Ala Phe Gly Arg Val Gly
324             145            150            155            160
326 Gly Leu Asn Cys Trp Glu His Phe Gln Pro Leu Ser Lys Phe Met Met
327             165            170            175
329 Tyr Ser Leu Gly Glu Gln Val His Val Ala Ser Trp Pro Ala Met Ser
330             180            185            190
332 Pro Leu Gln Pro Asp Val Phe Gln Leu Ser Ile Glu Ala Asn Ala Thr
333             195            200            205
335 Val Thr Arg Ser Tyr Ala Ile Glu Gly Gln Thr Phe Val Leu Cys Ser
336             210            215            220
338 Thr Gln Val Ile Gly Pro Ser Ala Ile Glu Thr Phe Cys Leu Asn Asp
339             225            230            235            240
341 Glu Gln Arg Ala Leu Leu Pro Gln Gly Cys Gly Trp Ala Arg Ile Tyr
342             245            250            255
344 Gly Pro Asp Gly Ser Glu Leu Ala Lys Pro Leu Ala Glu Asp Ala Glu

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VERIFICATION SUMMARY

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L:15 M:270 C: Current Application Number differs, Replaced Application Number
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date